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Result
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Maximum Match 100%
Listing first 45 summaries
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A; Molecule type: mRNA

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2) - upland cc ein; vicilin p d cotton) on 30-Sep-1991 A.B.; Dure III	A5.5%; SCOTE 1/5; DB 2; xal Similarity 32.4%; Pred. No. 1.4e-07; 33; Conservative 19; Mismatches 14; QRDPQQQYEQCQERCQRHETEPRHNOTCQORCERRYEKEKRK : : : : ERDPRQQYEQCQRRCESEATEEREQEOCERCEREYKEQORO	vision 30-Sep-1993 105; S22050 1992 ture and nucleotide :92288309 391/3; 502/1 n status predicted <8 s predicted <mat></mat>	ALIGNMENTS	A40691 S24548 S54522 A26892 H83273 B53234 B53234 B54024 F54024 F54024 E54024 E54024 E54024 E54024 B54024 B5
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Plant Mol
A; Title:
                                                                        N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
                                                                                                                                                         RESULT
S06398
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A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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A;Cross references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A:Fynorimental source: var. Coker 201
                                                          C; Accession:
                                                                                                                                    alpha-globulin type A precursor - upland cotton
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A; Accession: S08059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar
C;Accession: S08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Du:
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R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III,
Plant Mol. Biol. 9, 533-546, 1987
                                        R;Chlan, C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Developmental biochemistry of cottonseed embryogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
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A; Residues: 1-81 <CH2>
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A; Accession: S06911
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30; Conser
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                                        Borroto, K.;
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                                  Kamalay, J.A.;
                      1987
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Pred. No. 4.4e-05;
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embryogenesis
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germination.
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A;Reference number: S06398
A;Accession: S06398
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predic
                                        A; Molecule type: mRNA
                                                                            A; Accession: T44430
                                                                                                R:Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M. J. Biol. Chem. 274, 2503-2570, 1999
A:Title: Multiple functional proteins are produced A:Reference number: Z22767; MUID:99107919
                                                                                                                                                                        protein PV100 [imported] - winter squash C;Species: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Date: 21-Jul-430
                                                                                                                                                                                                                                                           T44430
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A; Mobile element:
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A;Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14390.1;
A;Experimental source: strain WS2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T02634
R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; H Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium disconnection nuclear plasmid Ddp5 is a chimera related to the Dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rep protein homolog - slime mold (Dictyostelium discoideum) plasmid Ddp5
C;Species: Dictyostelium discoideum
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1
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                        A; Residues: 1-810 < YAM>
                                                          A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: rep
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nes 25; Conser
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25; Conser
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EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1;
                                                          translated
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Pred. No. 0.00
18; Mismatches
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Pred. No. 0.0079; 
2; Mismatches 1
                                                              from
                                                                                                                                                        M.; Nishimura, M.;
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                                                            GB/EMBL/DDBJ
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PID:93808062

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R; Fietz, M.J.; Rogers, G.E.
submitted to the EMBL Data Library, December 1992
A; Description: Examination of the gene encoding rabbit trichohyalin.
A; Reference number: S28589
A; Accession: S28589
A; Molecule type: DNA
A; Residues: 1-147 <FIE>
A; Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747
C; Comment: Trichohyalin is a protein of the medulla of the hair and of the inner roo Covalent modifications to this protein include conversion of arginine to citrulline C; Genetics:
A; Introns: 46/3
                                                                                                                                                                                                                                                                      trichohyalin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 12-Mar-1993 #sequence_revision 01-Mar-1996 #text_change
C;Accession: S28589
R;Fietz, M.J.; Rogers, G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: DNA
A;Residues: 1-1898 <-LEE>
A;Residues: 1-1898 <-LEE>
A;Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichobyalin is a protein of the medulla of the hair and of the inner root
C;Comment: modifications to this protein include conversion of arginine to citrulline an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a funed (cross-linking) protein.
A;Reference number: A45973; MUID:93280194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
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C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair;
F;49-81/Domain: calmodulin repeat homology <EF2>
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C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
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Pred. No. 0.044;
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RESULT
T14004
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C;Species: Anopheles gambiae (African malaria mosquito)
C;Atte: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
submitted to the EMBL Data Library, June 1992
A;Bescription: Distinct families of site-specific retroposons occupy identical A;Reference number: S27770
A;Accession: S27770
A;Accession: S27770
                                                                                                                                                           A:Status: preliminary; translated
A:Molecule type: DNA
A:Residues: 1-1390 <SAI>
                                                                                                                                                                                                               A;Title: Dictyostelium TRFA homologous to yeast Ssn6 A;Reference number: 217852; MUID:98406112 A;Accession: T14004
                                                                                                                                                                                                                                                                                                      trfA protein - slime mold (Dictyostelium discoideum)
c;Specles: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #
C;Accession: T14004
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S27770
                                                                                          A; Introns:
                                                                                                         A;Gene: trfA
                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                     R;Saito, J.; Adachi, H.; Sutoh, K. J. Biol. Chem. 273, 24654-24659, 1998
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A;Residues: 1-613 <BES>
A;Cross·references: EMBL:M93690; NID:g159615; PID:g159616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                            A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1034109; PIDN:BAA33143.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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   Matches
                    Query Match
Best Local
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Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                     312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 EQEERREQRLEQEE 327
 Local Similarity hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 QQQLRRELEETREREQRLEQEERREQ--QLRREQRLEQEERREQQLRRELEETREREQRL 313
                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ERMKEEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 EDEEKYEERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYE
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                                                                                        333/3; 364/3; 637/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
27; Conser
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                    27.3%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.6%;
26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 110; DB
Pred. No. 0.06
19; Mismatches
                Score 105; DB Pred. No. 0.15;
                                                                                                                                                                                                from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106; DB 2
Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                       20-Sep-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
.06;
                                   2;
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 21;
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                                   Length 1390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 613
                                                                                                                                                                                                                                                    S
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                  required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RYEEQQR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
0,
                                                                                                                                                                                                                                                for normal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
Gaps
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0,
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A; molecule type: DNA
A; Residues: 1-385 <WIL>
A; Cross-references: EMBL: Z70204; PIDN: CAA94113.1; GSPDB: GN00028; CESP: C11G6.
                                                                                                                                                                                                                              A; Map position: X
A; Introns: 12/1; 106/3; 171/2; 335/2
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T19201
                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March 1996 A; Reference number: Z19089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C11G6.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: myoM
A;Map position: 6, aldB-cabA2
C;Superfamily: myosin motor domain homology
F;62-874/Domain: myosin motor domain homology #status atypical <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A59235
A;Accession: A59235
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1737 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum) c;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C;Accession: A59235
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A59235
                                                                                                                                                                                                                                                                         A; Gene: CESP:Cl1G6.3
                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T19201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \begin{array}{lll} \text{submitted to GenBank, September 1998} \\ \text{A;Description: Identification of two novel and highly divergent myosins in Dictyostelium} \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714396 A;Experimental source: strain AX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Geissler, H.; Schwarz, E.C.; Soldati,
                                                                                                                                              Query Match
Best Local S
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 NKRKEEERKKE--LER-QRKEEEERQKELERQRREEEKELERKRKEEERELERQRKEEEK 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 QQQQQQD 157
                                                                                                                           Local Similarity hes 20; Conserv
      53 QREDEEKYEERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 YEERMKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                2 RORDPOOQYEQCOERCORHETEPRHMO-----TCOORCERRYEKEKRKOOKRYEEO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NRQRDPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKE-KRKQQKRYEEQQREDEEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                          RERDERKERERQQKEKEREDAARREIEEKAEMDAKRVAEEEEERRKEKEKRREEKKKQKE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERMKEED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                               clone C11G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%;
                                                                                                                                              26.2%;
26.3%;
      83
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                                                                                                                      25; Mismatches
                                                                                                                                       Score 100.5; DE
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 105; DB 2
Pred. No. 0.18;
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                                                                                                                                                                 Length 385;
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                     RESULT
T30989
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Best Local Similarity
""" Conserve
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  serine/threonine
                                                                                                       Вþ
                                                                                                                                         Ωy
                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                      C; Genetics
A; Note: DKI
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1027 <ANA>
A;Cross-references: EMBL:AL137755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z23035
A; Accession: T46481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision
C:Accession: T46481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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A; Introns: 64/1; 154/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1995
A;Reference number: 219962
A;Accession: T24961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T18D3.1 - Caenorhabditis elegans c;Speciles: Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24961
                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: adult testis; clone DKF2p434A025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:T18D3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone T18D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z68119; PIDN:CAA92191.1; GSPDB:GN00028; CESP:T18D3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T24961
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Best Local Similarity
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                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 KEKDGHREEEKPKKKDKKHETE-----EERAER----KRKEKKEKERQERKEKEHDE 501
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                                          15
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                                                                                                                                                                                                                                                                                                                                                                      DKFZp434A025.1
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                                                                                                                                                                                                           RORDPQOQYEQCQ--ERCQRHETEPRHMQTCQQRCERRYEKEKRK----QQKRYEBQQR-54
                                                                                                     RAEEEKRRVEREQEYIRRQLEEE
                                                                                                                                         -----EDEEKYEERMKEED 68
                                                                                                                                                                                    RQKRIEQQKEQRRRLEEQQRREREARRQQEREQR--RREQEEKRRLEELERRRKEEEERR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.8%; ilarity 29.4%; Conservative 2:
protein kinase NIK -
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                        25.8%;
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                                                                                                                                                                                                                                                                                     Score 99; DB 2
Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; [
Pred. No. 0
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  mouse
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0.22;
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C:Species: Ms. masculus (Nouse mouse)
C:Cante: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: 73089
C:Accession: 73089
G:Bo. V.C.; Han. J.; Wi. S.; Cobb, M.; Skolnik, E.Y.
A:Beterence number: 220954 WHID:97280817
A:Scatter; Perliminary; translated from GB/EMBL/DDBJ
A:Scatter; Perliminary; Translated from GB/EMBL/DBBJ
A:Scatter; Perliminary; Translated from GB/EMBL/DB
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